SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
MENDELSOHN, FRED
CHAI, SIEW YEEN
MOELLER, INGRID
ALDRED, PETER
SMITH, IAN A
LEW, REBECCA A

(ii) TITLE OF INVENTION: NEUROACTIVE PEPTIDE

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: GRIFFITH HACK
(B) STREET: 509 ST KILDA ROAD
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3004

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: AU PO0893
(B) FILING DATE: 09-JUL-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: SANTER, VIVIEN B
(C) REFERENCE/DOCKET NUMBER: P21154

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: +61 3 9243 8300
(B) TELEFAX: +61 3 9243 8333/4

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Leu Val Val Thr Pro Thr Thr Gly Ala Pro
1 5
10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGGTTGTCT ACCCCTGGAC TCAGAG
26

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTGAGTCC AGGGGTAGAC AACCAG
26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTCAGGATCC ACATGCAGCT TATCACAG
28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGCACAACC ACTAGCACAT TGCC
24

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: not applicable

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAAACTCA GAAACAGACA CCATGGTGCA CCTGAGTGCT TCTGACATAG
TTGTGTTGAC 60

TCACAAACTC AGAAACAGAC ACCATGGTGC ACCTGACTGA TGCTGAGAAG
GCTGCTGTTA 120

ATGGCCTGTG GGGAAAGGTG AACCCTGATG ATGTTGGCTG ATGCTGAGAA
GGCTGCTGTT 180

AATGGCCTGT GGGGAAAGGT GAACCCTGAT GATGTTGGTG GCGAGGCCCT
GGGCAGGCTG 240

CTGGTTGTCT ACCCTTGGAC CCAGAGGTAC TTTGATAGGT GGCGAGGCCC
TGGGCAGGCT 300

GCTGGTTGTC TACCCTTGGA CCCAGAGGTA CTTTGATAGC TTTGGGGACC
TGTCCTCTGC 360

CTCTGCTATC ATGGGTAACC CTAAGGTGAA GGCCCATGGG CTTTGGGGAC
CTGTCCTCTG 420

CCTCTGCTAT CATGGGTAAC CCTAAGGTGA AGGCCCATGG CAAGAAGGTG
ATAAACGCCT 480

TCAATGATGG CCTGAAACAC TTGGACAACC TCAAGGGCAG GCAAGAAGGT
GATAAACGCC 540

TTCAATGATG GCCTGAAACA CTTGGACAAC CTCAAGGGCA CCTTTGCTCA
TCTGAGTGAA 600

CTCCACTGTG ACAAGCTGCA TGTGGATCCT GAGAACTTCA GCCTTTGCTC
ATCTGAGTGA 660

ACTCCACTGT GACAAGCTGC ATGTGGATCC TGAGAACTTC AGGCTCCTGG
GCAATATGAT 720

TGTGATTGTG TTGGGCCACC ACCTGGGCAA GGAATTCACC CGGGCTCCTG
GGCAATATGA 780

TTGTGATTGT GTTGGGCCAC CACCTGGGCA AGGAATTCAC CCCCTGTGCA
CAGGCTGCCT 840

TCCAGAAGGT GGTGGCTGGA GTGGCCAGTG CCCTGGCTCA CAGCCTGTGC
ACAGGCTGCC 900

TTCCAGAAGG TGGTGGCTGG AGTGGCCAGT GCCCTGGCTC ACAAGTACCA
CTAAACCTCT 960

TTTCCTGCTC TTGTCTTTGT GCAATGGTCA ATTGTTCCCA AGAGAGTACC
ACTAAACCTC 1020

TTTTCCTGCT CTTGTCTTTG TGCAATGGTC AATTGTTCCC AAGAGAGCAT
CTGTCAGTTG 1080

TTGTCAAAAT GACAAAGACC TTTGAAAATC TGTCCTACTA ATAAGGAGCA
TCTGTCAGTT 1140

Sub B1 cont

GTTGTCAAAA TGACAAAGAC CTTTGAAAAT CTGTCCTACT AATAAAAGGC ATTTACTTTC 1200

ACTGCAAAAA AAAAAAAAAA AAAGAAGGCA TTTACTTTCA CTGC 1244

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 649 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACAAACTCA GAAACAGACA CCATGGTGCA CCTGACTGAT GCTGAGAAGG CTGCTGTTAA 60

TGGCCTGTGG GGAAAGGTGA ACCCTGATGA TGTTGTAAAG GGTGGCGAGG CCCTGGGCAG 120

GCTGCTGGTT GTCTACCCTT GGACCCAGAG GTACTTTGAT AGGAGTGCTT TGGGGACCTG 180

TCCTCTGCCT CTGCTATCAT GGGTAACCCT AAGGTGAAGG CCCATGGAAG AGCAAGAAGG 240

TGATAAACGC CTTCAATGAT GGCCTGAAAC ACTTGGACAA CCTCAAGGGC AGAGGCCTTT 300

GCTCATCTGA GTGAACTCCA CTGTGACAAG CTGCATGTGG ATCCTGAGAA CTTCATACGG 360

CTCCTGGGCA ATATGATTGT GATTGTGTTG GGCCACCACC TGGGCAAGGA ATTCACCCGG 420

GTCCTGTGCA CAGGCTGCCT TCCAGAAGGT GGTGGCTGGA GTGGCCAGTG CCCTGGCTCA 480

CACAAAAGAA AAGTACCACT AAACCTCTTT TCCTGCTCTT GTCTTTGTGC AATGGTCAAT 540

TGTTCCCAAG AGAGCATCTG TCAGTTGTTG TCAAAATGAC AAAGACCTTT GAAAATCTGT 600

CCTACTAATA AAAGGCATTT ACTTTCACTG CAAAAAAAAA AAAAAAAAA
649

Sub B1 cont